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Reviewer: Anne Corrigan

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Application No:	10582549	Version No:	1.1
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No. of SeqIDs Defined:	4
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# SUBSTITUTE SEQUENCE LISTING

<110> The Regents of the University of Michigan

<120> Geraniol Synthase, Method of Production and Uses Thereof

<130> 2115-002692

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<141> 2009-08-21

<150> PCT/US2004/040321

<151> 2004-12-02

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<170> PatentIn version 3.5

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<301> Iijima,Y., Gang,D.R., Lewinsohn,E. and Pichersky,E.

<302> Characterization of geraniol synthase from the peltate glands of sweet basil

<303> Plant Physiol.

<304> 134

<305> 1

<306> 370-379

<307> 2004

<308> AY362553

<309> 2004-08-05

<313> (1)..(1704)

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Thr	Thr	Arg	Lys	Leu	Gln	Arg	Asn	Asp	Thr	Glu	Ser	Val	Glu	Lys	Leu	
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Lys	Leu	Ile	Asp	Asn	Ile	Gln	Gln	Leu	Gly	Ile	Gly	Tyr	Tyr	Phe	Glu	
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Asp	Ala	Ile	Asn	Ala	Val	Leu	Arg	Ser	Pro	Phe	Ser	Thr	Gly	Glu	Glu	
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Asp	Leu	Phe	Thr	Ala	Ala	Leu	Arg	Phe	Arg	Leu	Leu	Arg	His	Asn	Gly	
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Lys	Phe	Asp	Glu	Ser	Asp	Thr	Leu	Gly	Leu	Leu	Ser	Leu	Tyr	Glu	Ala	
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Pro	Leu	Glu	Cys	Phe	Leu	Trp	Thr	Val	Gly	Leu	Leu	Pro	Glu	Pro	Lys	290	295	300
Tyr	Ser	Ser	Val	Arg	Ile	Glu	Leu	Ala	Lys	Ala	Ile	Ser	Ile	Leu	Leu	305	310	315
Val	Ile	Asp	Asp	Ile	Phe	Asp	Thr	Tyr	Gly	Glu	Met	Asp	Asp	Leu	Ile	325	330	335
Leu	Phe	Thr	Asp	Ala	Ile	Arg	Arg	Trp	Asp	Leu	Glu	Ala	Met	Glu	Gly	340	345	350
Leu	Pro	Glu	Tyr	Met	Lys	Ile	Cys	Tyr	Met	Ala	Leu	Tyr	Asn	Thr	Thr	355	360	365
Asn	Glu	Val	Cys	Tyr	Lys	Val	Leu	Arg	Asp	Thr	Gly	Arg	Ile	Val	Leu	370	375	380
Leu	Asn	Leu	Lys	Ser	Thr	Trp	Ile	Asp	Met	Ile	Glu	Gly	Phe	Met	Glu	385	390	395
Glu	Ala	Lys	Trp	Phe	Asn	Gly	Gly	Ser	Ala	Pro	Lys	Leu	Glu	Glu	Tyr	405	410	415
Ile	Glu	Asn	Gly	Val	Ser	Thr	Ala	Gly	Ala	Tyr	Met	Ala	Phe	Ala	His	420	425	430
Ile	Phe	Phe	Leu	Ile	Gly	Glu	Gly	Val	Thr	His	Gln	Asn	Ser	Gln	Leu	435	440	445
Phe	Thr	Gln	Lys	Pro	Tyr	Pro	Lys	Val	Phe	Ser	Ala	Ala	Gly	Arg	Ile	450	455	460
Leu	Arg	Leu	Trp	Asp	Asp	Leu	Gly	Thr	Ala	Lys	Glu	Glu	Gln	Glu	Arg	465	470	475
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490

495

Thr

Glu

Glu

Glu

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Trp

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Asp

Ser

Ile

Gln

Arg

Leu

Glu

Leu

Ile

100

105

110

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115 120 125

Val Glu Ile Leu Asn Ser Lys Tyr Tyr Thr Asn Asn Glu Ile Asp Glu  
130 135 140

Ser Asp Leu Tyr Ser Thr Ala Leu Arg Phe Lys Leu Leu Arg Gln Tyr  
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Asp Phe Ser Val Ser Gln Glu Val Phe Asp Cys Phe Lys Asn Asp Lys  
165 170 175

Gly Thr Asp Phe Lys Pro Ser Leu Val Asp Asp Thr Arg Gly Leu Leu  
180 185 190

Gln Leu Tyr Glu Ala Ser Phe Leu Ser Ala Gln Gly Glu Glu Thr Leu  
195 200 205

His Leu Ala Arg Asp Phe Ala Thr Lys Phe Leu His Lys Arg Val Leu  
210 215 220

Val Asp Lys Asp Ile Asn Leu Leu Ser Ser Ile Glu Arg Ala Leu Glu  
225 230 235 240

Leu Pro Thr His Trp Arg Val Gln Met Pro Asn Ala Arg Ser Phe Ile  
245 250 255

Asp Ala Tyr Lys Arg Arg Pro Asp Met Asn Pro Thr Val Leu Glu Leu  
260 265 270

Ala Lys Leu Asp Phe Asn Met Val Gln Ala Gln Phe Gln Gln Glu Leu  
275 280 285

Lys Glu Ala Ser Arg Trp Trp Asn Ser Thr Gly Leu Val His Glu Leu  
290 295 300

Pro Phe Val Arg Asp Arg Ile Val Glu Cys Tyr Tyr Trp Thr Thr Gly  
305 310 315 320

Val Val Glu Arg Arg Glu His Gly Tyr Glu Arg Ile Met Leu Thr Lys  
325 330 335



Ile Asn Ala Leu Val Thr Thr Ile Asp Asp Val Phe Asp Ile Tyr Gly  
340 345 350

Thr Leu Glu Glu Leu Gln Leu Phe Thr Thr Ala Ile Gln Arg Trp Asp  
355 360 365

Ile Glu Ser Met Lys Gln Leu Pro Pro Tyr Met Gln Ile Cys Tyr Leu  
370 375 380

Ala Leu Phe Asn Phe Val Asn Glu Met Ala Tyr Asp Thr Leu Arg Asp  
385 390 395 400

Lys Gly Phe Asn Ser Thr Pro Tyr Leu Arg Lys Ala Trp Val Asp Leu  
405 410 415

Val Glu Ser Tyr Leu Ile Glu Ala Lys Trp Tyr Tyr Met Gly His Lys  
420 425 430

Pro Ser Leu Glu Glu Tyr Met Lys Asn Ser Trp Ile Ser Ile Gly Gly  
435 440 445

Ile Pro Ile Leu Ser His Leu Phe Phe Arg Leu Thr Asp Ser Ile Glu  
450 455 460

Glu Glu Asp Ala Glu Ser Met His Lys Tyr His Asp Ile Val Arg Ala  
465 470 475 480

Ser Cys Thr Ile Leu Arg Leu Ala Asp Asp Met Gly Thr Ser Leu Asp  
485 490 495

Glu Val Glu Arg Gly Asp Val Pro Lys Ser Val Gln Cys Tyr Met Asn  
500 505 510

Glu Lys Asn Ala Ser Glu Glu Glu Ala Arg Glu His Val Arg Ser Leu  
515 520 525

Ile Asp Gln Thr Trp Lys Met Met Asn Lys Glu Met Met Thr Ser Ser  
530 535 540

Phe Ser Lys Tyr Phe Val Gln Val Ser Ala Asn Leu Ala Arg Met Ala  
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Leu Leu Ser Ser Thr Asn Ser Ser Ser Arg Ser Arg Leu Arg Val Tyr					
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Cys Ser Ser Ser Gln Leu Thr Thr Glu Arg Arg Ser Gly Asn Tyr Asn					
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Pro Ser Arg Trp Asp Val Asn Phe Ile Gln Ser Leu Leu Ser Asp Tyr					
65		70		75	80
Lys Glu Asp Lys His Val Ile Arg Ala Ser Glu Leu Val Thr Leu Val					
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Lys Met Glu Leu Glu Lys Glu Thr Asp Gln Ile Arg Gln Leu Glu Leu					
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Ile Asp Asp Leu Gln Arg Met Gly Leu Ser Asp His Phe Gln Asn Glu					
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	130		135		140
Asn Pro Phe Pro Lys Glu Glu Arg Asp Leu Tyr Ser Thr Ser Leu Ala					
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Phe Arg Leu Leu Arg Glu His Gly Phe Gln Val Ala Gln Glu Val Phe					
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Cys	Tyr	Phe	Trp	Asn	Thr	Gly	Ile	Ile	Glu	Pro	Arg	Gln	His	Ala	Ser
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Arg Gln Ser Trp Val Asp Leu Ala Asp Lys Tyr Met Val Glu Ala Arg  
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Arg Val Thr Asp Ser Phe Thr Lys Glu Thr Val Asp Ser Leu Tyr Lys  
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Tyr His Asp Leu Val Arg Trp Ser Ser Phe Val Leu Arg Leu Ala Asp  
485 490 495

Asp Leu Gly Thr Ser Val Glu Glu Val Ser Arg Gly Asp Val Pro Lys  
500 505 510

Ser Leu Gln Cys Tyr Met Ser Asp Tyr Asn Ala Ser Glu Ala Glu Ala  
515 520 525

Arg Lys His Val Lys Trp Leu Ile Ala Glu Val Trp Lys Lys Met Asn  
530 535 540

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